

**In the Specification:**

Please amend the specification as follows:

Please replace the paragraph beginning at page 7, line 30 (spanning pages 7-8), with the following re-written paragraph:

*C3*  
Figure 4B is a depiction of regions of homology between the predicted sequence of RDE-1 and four related proteins. The sequences are RDE- 1 (*C elegans*; Genbank Accession No. AF180730) (SEQ ID NO:13), F48F7.1 (*C elegans*; Genbank Accession No. Z69661) (SEQ ID NO:9), eIF2C (rabbit; Genbank Accession No. AF005355) (SEQ ID NO: 10), ZWILLE (*Arabidopsis*; Genbank Accession No. AJ223508) (SEQ ID NO:6), and Sting (*Drosophila*; Genbank Accession No. AF145680) (SEQ ID NO:7). Identities with RDE- 1 are shaded in black, and identities among the homologs are shaded in gray.

Please replace the paragraph beginning at page 9, line 6, with the following re-written paragraph:

*C4*  
Figure 11 is a depiction of regions of homology between the predicted RDE-4 amino acid sequence (SEQ ID NO:14), X1RBPA (SEQ ID NO:11), HsPKR (SEQ ID NO:12), and a consensus sequence (SEQ ID NO:8). A predicted secondary structure for RDE-4 is also shown illustrating predicted regions of  $\alpha$  helix and  $\beta$  pleated sheet.

Please replace the paragraph beginning at page 47, line 14, with the following re-written paragraph:

*C5*  
Analysis of the *rde-4* nucleic acid sequence shows that it encodes a protein (RDE-4) with similarities to dsRNA binding proteins. Examples of the homology to X1RBPA (SEQ ID NO:11; Swissprot: locus \_TRBP\_XENLA, accession Q91836; Eckmann and Jantsch, 1997, J. Cell Biol. 138:239-253) and HSPKR (SEQ ID NO:12; AAF13156.1; Xu and Williams, 1998, J. Interferon Cytokine Res. 18:609-616), and a consensus sequence (SEQ ID NO:8) are shown in Fig. 11. Three regions have been identified within the predicted RDE-4 protein corresponding to conserved regions found in all members of this dsRNA binding domain family. These regions appear to be important for proper folding

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COO<sup>t</sup>

of the dsRNA binding domain. Conserved amino acid residues, important for interactions with the backbone of the dsRNA helix, are found in all members of the protein family including RDE-4 (see consensus residues in Figure 11). This motif is thought to provide for general non-sequence-specific interactions with dsRNA. The RDE-4 protein contains conserved protein folds that are thought to be important for the assembly of the dsRNA binding domain in this family of proteins. Conserved amino acid residues in RDE-4 are identical to those that form contacts with the dsRNA in the crystal structure of the XIRBP dsRNA complex. These findings strongly suggest that RDE-4 is likely to have dsRNA binding activity.